Phoowanarth Maneechoat 2010: Biodiversity of *Cucumber mosaic virus* Isolated from Cucumber in Thailand. Master of Science (Agriculture), Major Field: Plant Phatology, Department of Plant Pathology. Thesis Advisor: Assistant Professor Pissawan Chiemsombat, Dr.Agr. 103 pages.

Cucumber mosaic virus (CMV) is one of the most important plant viruses infecting several economic crops including cucurbitaceous plants. This study aimed to explore the diversity of CMV isolated from cucumber to support breeding program for virus resistance. The total 2,250 samples were collected from fields in 11 provinces and 4 samples were positively assayed for CMV infection by indirect PTA-ELISA. These 4 isolates together with 6 received isolates were used in biodiversity study. All isolates were separately purified from 50 g tobacco leaf tissues and yielded about 0.340-1.680 mg virus. Virus particles were icosahedra shaped size of 24-28 nm. Virion coat protein (CP) M.W. was estimated to be 26 kDa. CMV multiplication and translocation started from the inoculated tobacco leaves to the upper leaves via vascular cells of midvein and veinlet through the whole area of leaf blade parenchyma cells during 4-13 days post inoculation. *Vigna radiata* was a good local lesion host for virus isolation. Infected *Cucumis sativus* cv. Poomchaba showed mild symptom or symptomless leaves while *Nicotiana* spp., *Datura metel*, *Physalis angulata*, *Capsicum annuum*, and *Solanum lycopersicum* developed severe mosaic with leaf distortion. Responses of *C.annuum* cv. Huarua and *S.lycopersicum* cv. Seedatip4 to CMV slightly varied among virus isolates but infection percentage varied from 10 to100%. Analysis of nucleotide and amino acid sequences followed by multiple alignments indicated the same structure of 2b, CP genes and 3' NTR of all cucumber isolates. Nucleotide and amino acid sequences shared about 89-100% and 85-100% identities for 2b gene, 89%-99% and 92%-100% for CP gene, and 91%-100% for 3' NTR, respectively. Isolates HC53, HC56 and CRI, including A168 were the most closed strains. Sequence diversity was present in CP more than 2b genes. Phylogenetic analysis placed all Thai CMV isolates in subgroup IB. Thai isolates from cucumber and pepper clustered together except isolates SNK, PBR and SK211. No correlation between sampling location to sequence diversity was found.

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